

AMENDMENTS

IN THE CLAIMS:

Please amend claims 47, 61 and 64 as follows:

E 1
47. (three times amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a selectable or screenable marker gene selected from the group of genes consisting of [a dalapon dehalogenase (*deh*) gene; an anthranilate synthase gene that confers resistance to 5 methyl tryptophan;] an aequorin gene and a gene encoding a cell wall protein, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

E 12
61. (twice amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising an exogenous gene encoding a selected trait, the gene positioned under the control of an inducible or tissue-specific promoter or enhancer comprising an α -tubulin promoter, [an actin promoter,] an *ocs* promoter, an ABA-inducible promoter, or a turgor-inducible promoter, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

64. (twice amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding [a disease resistance trait selected from the group of genes consisting of a cecropin gene; a magainin gene; and] a pathogenesis related (PR) protein gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

Please cancel claim 59, without prejudice.

67. (twice amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a grain composition trait selected from the group of genes consisting of [an aspartokinase gene;] an acetyl-CoA carboxylase gene; an ACP-acyltransferase gene; a β -ketoacyl-ACP synthase gene; an acyl carrier protein gene; a fatty acid desaturase gene; a fatty acid epoxidase gene; a fatty acid hydratase gene; a fatty acid dehydratase gene; a sense or antisense phytoene synthase gene; a sense or antisense phytoene desaturase gene; a sense or antisense lycopene synthase gene; a ~~phytase~~ gene; an ADP-glucose pyrophosphorylase gene; a starch synthase gene; a starch branching enzyme gene; and a sucrose synthase gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is